

Supplementary Data

Supplementary Information

Gene expression analysis

A further search for relationships to gene sets in curated pathways and sets affected by genetic and chemical perturbations (from the publicly available Molecular Signatures Database) was done with Gene Set Enrichment Analysis (GSEA) [1]. GSEA indicated that genes upregulated in aryl hydrocarbon receptor (AhR)-KO cells were enriched for genes in the following sets: human18S U11/U12 sn RNP [2,3], gene altered in endothelial cells in response to oxidized phospholipids [4], expression signature for cases of acute myelogenous leukemia [5] genes differentially expressed in human thymus compared to other tissues [6]. The changes in enrichment of downregulated genes in AhR-KO mice was also compared with the following published genes sets: differentially expressed genes in human peripheral lymphocytes in response to aging and heat shock [7], genes involved in the regulation of adult germline stem cells [8], genes involved in the Wnt canonical pathway and β -catenin degradation [9].

Supplementary References

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